

SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANT:

(A) NAME: RHONE-POULENC RORER S.A.

5 (B) STREET: 20, avenue Raymond ARON

(C) CITY: ANTONY

(E) COUNTRY: FRANCE

(F) POSTAL CODE: 92165

## (ii) TITLE OF INVENTION: NOVEL TOPOISOMERASE IV,

10 CORRESPONDING NUCLEOTIDE SEQUENCES AND USES.

## (iii) NUMBER OF SEQUENCES: 14

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: tape

(B) COMPUTER: IBM PC compatible

15 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0,

Version #1.25 (EPO)

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 4565 base pairs

(B) TYPE: nucl ic acid

(C) STRANDEDNESS: doubl

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

5

(A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

10	20	30	40	50	60
GAATTCGAC	GTACGTTTG	AGGAGGCGAA	ATCATTGGCA	ATGAATAAAC	AAAATAATTA
CTTAAGGCTG	CATGCAAACG	TCCTCCGCTT	TAGTAACCGT	TACTTATTTG	TTTATTAAAT
70	80	90	100	110	120
TTCAGATGAT	TCAATACAGG	TTTtagaggg	GTTAGAAGCA	GTTCGTAAAA	GACCTGGTAT
AAGTCTACTA	AGTTATGTCC	AAAATCTCCC	CAATCTTCGT	CAAGCATTIT	CTGGACCATA
130	140	150	160	170	180
GSTATATTGA	TCAACTGATA	AACGGGGATT	ACATCATCTA	GTATATGAAA	TTGTCGATAA
CATATAACCT	AGTTGACTAT	TTGCCCCCTAA	TGTAGTAGAT	CATATACTTT	AACAGCTATT

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190      200      210      220      230      240
CTCCGTCGAT GAAGTATTGA ATGGTTACGG TAACGAAATA GATGTAACAA TTAATAAAGA
GAGGCAGCTA CTTCATAACT TACCAATGCC ATTGCTTTAT CTACATTGTT AATTATTTCT

250      260      270      280      290      300
TGGTAGTATT TCTATAGTAG ATAATGGACG TGGTATGCCA ACAGGTATAC ATAAATCAGG
ACCATATATA AGATATCTTC TATTACCTGC ACCATACGGT TGTCCATATG TATTTAGTCC

310      320      330      340      350      360
TAAACCTACA GTGGAAGTTA TCTTTACTGT TTTACATGCA GGAGGTAAAT TTGGACAAGG
ATTTGGCTGT CAGCTTCAAT AGAAATGACA AAATGTACGT CCTCCATTTA AACCTGTTCC

370      380      390      400      410      420
TGGCTATAAA ACTTCAGGTG GTCTTCACGG CGTTGGTGCT TCAAGTGTAA ATGCATTGAG
ACCGATATTT TGAAGTCCAC CAGAAGTGCC GCAACCACGA AGTCACCATT TACGTAACTC

430      440      450      460      470      480
TGAATGGCTT GAAGTTGAAA TCCATCGAGA TGGTAATATA TATCATCAAA GTTTTAAAAA
ACTTACCGAA CTTCACTTTT AGGTAGCTCT ACCATTATAT ATAGTAGTTT CAAAATTTTT

490      500      510      520      530      540
CGGTGGTTCC CCATCTTCAG GTTTAGTGAA AAAAGGTAAA ACTAAGAAAA CAGGTACCAA
GCCACCAAGC GGTAGAAGTC CAAATCACTT TTTTCCATTT TGATTTCTTT GTCCATGGTT

550      560      570      580      590      600
AGTAACATTT AAACCTGATG ACACAATTTT TAAAGCATCT ACATCATTTA ATTTTGATGT
TCATTGTAAA TTTGGACTAC TGTGTTAAAA ATTTGCTAGA TGTAGTAAAT TAAACTACA

610      620      630      640      650      660
TTTAAGTGAA CGACTACAAG AGTCTGCGTT CTTATTGAAA AATTTAAAAA TAACGCTTAA
AAATTCATT GCTGATGTTT TCAGACGCAA GAATAACTTT TTAATTTTTT ATTGCGAATT

670      680      690      700      710      720
TGATTTACGC AGTGGTAAAG AGCGTCAAGA GCATTACCAT TATGAAGAAG GAATCAAAGA
ACTAAATGCG TCACCATTTC TCGCAGTTCT CGTAATGGTA ATACTTCTTC CTTAGTTTCT

730      740      750      760      770      780
GTTTGTTAGT TATGTCAATG AAGGAAAAGA AGTTTTGCAT GACGTGGCTA CATTITCAGG
CAACAATCA ATACAGTTAC TTCCTTTTCT TCAAAACGTA CTGCACEGAT GTAAAAGTCC

790      800      810      820      830      840
TGAAGCAAAAT GGTATAGAGG TAGACGTAGC TTTCCAATAT AATGATCAAT ATTCAGAAAG
ACTTCGTTTA CCATATCTCC ATCTGCATCG AAAGGTTATA TTACTAGTTA TAAGTCTTTC

850      860      870      880      890      900
TATTTTAAAG TTTGTAATA ATGTACGTAC TAAAGATGGT GGTACACATG AAGTTGGTTT
ATAAAATTCA AAACATTTAT TACATGCATG ATTTCTACCA CCATGTGTAC TTCAACCAA

910      920      930      940      950      960
TAAACACGCA ATGACACGCG TATTTAATGA TTATGCACGT CGTATTAATG AACTTAAAC
ATTTGTCTGT TACTGTGCGC ATAAATTACT AATACGTGCA GCATAATTAC TTGAATTTTG

970      980      990      1000      1010      1020
AAAAGATAAA AACTTAGATG GTATATGATAT TCGTGAAGGT TTAACAGCTG TTGTGTCTGT
TTTCTATTT TTGAATCTAC CATTACTATA AGCACTTCCA AATTGTGAC AACACAGACA

1030      1040      1050      1060      1070      1080
TCGTATTCCA GAAGAATTAT TGCAATTTGA AGGACAAACG AAATCTAAAT TGGGTACTTC
AGCATAAGGT CTTCTTAATA ACGTTAAACT TCCTGTTTGC TTTAGATTTA ACCCATGAAG

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1090	1100	1110	1120	1130	1140
TGAAGCTAGA	AGTGCTGTTG	ATTCAGTTGT	TGCAGACAAA	TTGCCATTCT	ATTTAGAAGA
ACTTCGATCT	TCACGACAAC	TAAGTCAACA	ACGTCTGTTT	AACGGTAAGA	TAAATCTTCT
1150	1160	1170	1180	1190	1200
AAAAGGACAA	TTGTCTAAAT	CAC TTGTGAA	AAAAGCGATT	AAAGCACAAC	AAGCAAGGGA
TTTTCCTGTT	AACAGATTTA	GTGAACACTT	TTTTCGCTAA	TTTCGTGTTG	TTCTGTTCCCT
1210	1220	1230	1240	1250	1260
AGCTGCACGT	AAAGCTCGTG	AAGATGCTCG	TTCAGGTAAG	AAAAAGCAGC	GTAAAGACAC
TCGACGTGCA	TTTCGAGCAC	TTCTACGAGC	AAGTCCATTC	TTTTTGTTCC	CATTTCTGTG
1270	1280	1290	1300	1310	1320
TTTGCTATCT	GGTAAATTAA	CACCTGCACA	AAGTAAAAAC	ACTGAAAAAA	ATGAATTGTA
AAACGATAGA	CCATTAAATT	GTGGACGTGT	TTCATTTTTC	TGACTTTTTT	TACTTAACAT
1330	1340	1350	1360	1370	1380
TTTAGTCGAA	GGTGATTCTG	CGGGAGGTTT	AGCAAACTT	GGACGAGACC	GCAAATTCCA
AAATCAGCTT	CCACTAAGAC	GCCCTCCAAG	TCGTTTTGAA	CCTGCTCTGG	CGTTTAAGGT
1390	1400	1410	1420	1430	1440
AGCGATATTA	CCATTACGTG	GTAAAGTAAT	TAATACAGAG	AAAGCACGTC	TAGAAAGATAT
TCGCTATAAT	GGTAATGCAC	CATTCCATTA	ATTATGTCTC	TTTCGTGCAG	ATCTTCTATA
1450	1460	1470	1480	1490	1500
TTTTAAAAAT	GAAGAAATTA	ATACAATTAT	CCACACAATC	GGGGCAGGCG	TTGGTACTGA
AAAATTTTAA	CTTCTTTAAT	TATGTTAATA	GGTGTGTTAG	CCCCGTCCCG	AACCATGACT
1510	1520	1530	1540	1550	1560
CTTTAAAAAT	GAAGATAGTA	ATTATAATCG	TGTAATTATT	ATGACTGATG	CTGATACTGA
GAAATTTTAA	CTTCTATCAT	TAATATTAGC	ACATTAAATA	TACTGACTAC	GACTATGACT
1570	1580	1590	1600	1610	1620
TGGTGCGCAT	ATTCAAGTGC	TATTGTTAAC	ATTCTTCTTC	AAATATATGA	AACCGCTTGT
ACCACGCGTA	TAAGTTCACG	ATAACAATTG	TAAGAAGAAG	TTATATATACT	TTGGCGAACA
1630	1640	1650	1660	1670	1680
TCAAGCAGGT	CGTGTAATTA	TTGCTTTACC	TCCACTTTAT	AAATTGGAAA	AAGGTAAAGG
AGTTTCGTCCA	GCACATAAAT	AACGAAATGG	AGGTGAAATA	TTTAACCTTT	TTCCATTTC
1690	1700	1710	1720	1730	1740
CAAAACAAAG	CGAGTTGAAT	ACGCTTGGAC	AGACGAAGAG	CTTAATAAAT	TGCAAAAAGA
GTTCCTGTTT	GCTCAACTTA	TGCGAACCTG	TCTGCTTCTC	GAATTATTTA	ACGTTTTTCT
1750	1760	1770	1780	1790	1800
ACTTGGTAAA	GGCTTCACGT	TACAACGTTA	CAAAGGTTTG	GGTGAAATGA	ACCTGGAACA
TGAACCTTTT	CCGAAGTGCA	ATGTTGCAAT	GTTTCCTAAC	CCACTTTIAC	TGGGACTTGT
1810	1820	1830	1840	1850	1860
ATTATGGGAA	ACGACGATGA	ACCCAGAAAC	ACGAACCTTA	ATTCGTGTAC	AAGTTGAAGA
TAATACCCTT	TGCTGCTACT	TGGGTCTTTG	TGCTTGAAAT	TAAGCACATG	TTCAACTTCT
1870	1880	1890	1900	1910	1920
TGAAGTGCGT	TCATCTAAAC	GTGTAACAAC	ATTAATGGGT	GACAAAGTAC	AACCTAGACG
ACTTCACGCA	AGTAGATTTC	CACATTGTTG	TAATTACCCA	CTGTTTCATG	TTGGATCTGC

1930	1940	1950	1960	1970	1980
TGAATGGATT	GAAGAGCATG	TTGAGTTTGG	TATGCAAGAG	GACCAAAGTA	TTTTAGATAA
ACTTACGTAA	CTTTTCGTAC	AACTCAAACC	ATACGTTCTC	CTGGTTTCAT	AAAATCTATT
1990	2000	2010	2020	2030	2040
TTCTGAAGTA	CAAGTGCTTG	AAAATGATCA	ATTTGATGAG	GAGGAAATCT	AGTGAGTGAA
AAGACTTCAT	GTTACGGAAC	TTTTACTAGT	TAAACTACTC	CTCCTTTAGA	TCACTCACTT
2050	2060	2070	2080	2090	2100
ATAATTCAAG	ATTTATCACT	TGAAGATGTT	TTAGGTGATC	GCTTTGGAAG	ATATAGTAAA
TATTAAGTTC	TAAATAGTGA	ACTTCTACAA	AATCCACTAG	CGAAACCTTC	TATATCATT
2110	2120	2130	2140	2150	2160
TATATTATTC	AAGAGCGTGC	ATTGCCAGAT	GTTCTGTGATG	GTTTAAACC	AGTACAACGT
ATATAATAAG	TTCTCGCAGG	TAACGGCTTA	CAAGCACTAC	CAAAATTTTG	TCATGTTGCA
2170	2180	2190	2200	2210	2220
CGTATTTTAT	ACGCAATGTA	TTCAAGTGCT	AATACACACG	ATAAAATTT	CCGTAAAGT
GCATAAAATA	TGCGTTACAT	AAGTTCACCA	TTATGTGTGC	TATTTTTAAA	GGCATTTTCA
2230	2240	2250	2260	2270	2280
GCGAAACAG	TGGGTGATGT	TATTGGTCAA	TATCATCCAC	ATGGAGACTC	CACAGTGATC
CGCTTTTGTC	AGCCACTACA	ATAACCACTT	ATAGTAGGTG	TACCTCTGAG	GAGTCACATC
2290	2300	2310	2320	2330	2340
GAAGCAATGG	TCCGTTTAAG	TCAAGACTGG	AAGTTALGAC	ATGTCTTAAT	AGAAATGCAT
CTTCGTTACC	AGGCAAAATC	AGTTCTGACC	TTCAATGCTG	TACAGAAATTA	TCTTTACGTA
2350	2360	2370	2380	2390	2400
GGTAATAATG	GTAGTATCGA	TAATGATCCG	CCAGCGGCAA	TGCGTTACAC	TGAAGCTAAG
CCATTATTAC	CATCATAGCT	ATTACTAGGC	GGTCGCTTTT	ACGCAATGTC	ACTTCGATTC
2410	2420	2430	2440	2450	2460
TTAAGCTTAC	TAGCTGAAGA	GTTATTACGT	GATATTAATA	AAGAGACAGT	TTCTTTCAAT
AATTCGAATG	ATCGACTTCT	CAAGAATGCA	CTATAATTAT	TTCTCTGTCA	AAGAAAGTAA
2470	2480	2490	2500	2510	2520
CCAAACTATG	ATGATACGAC	ACTCGAACCA	ATGGTATTGC	CATCAAGATT	TCCTAACTTA
GGTTTGATAC	TACTATGCTG	TGAGCTTGGT	TACCATAACG	GTAGTTCTAA	AGGATTGAAT
2530	2540	2550	2560	2570	2580
CTAGTGAATG	GTTCTACAGG	TATATCTGCA	GGTTACGCGA	CAGATATACC	ACCACATAAT
GATCACTTAC	CAAGATGTCC	ATATAGACGT	CCAATGCGCT	GTCTATATGG	TGGTGTATTA
2590	2600	2610	2620	2630	2640
TTAGCTGAAG	TGATTCAAGC	AACACTTAAA	TATATTGATA	ATCCGGATAT	TACAGTCAAT
AATCGACTTC	ACTAAGTTCG	TTGTGAATTT	ATATAACTAT	TAGGCCTATA	ATGTCAGTTA
2650	2660	2670	2680	2690	2700
CAATTAATGA	AATATATTAA	AGGTCCTGAT	TTTCCAACCTG	GTGGTATTAT	TCAAGGTATT
GTTAATTACT	TTATATAATT	TCCAGGACTA	AAAGGTTGAC	CACCATAATA	AGTTCCATAA
2710	2720	2730	2740	2750	2760
GATGGTATTA	AAAAAGCTTA	TGAATCAGGT	AAAGGTAGAA	TTATAGTTCTG	TTCTAAAGTT
CTACCATAAT	TTTTTCGAAT	ACTTAGTCCA	TTTCCATCTT	AATATCAAGC	AAGATTTCAA
2770	2780	2790	2800	2810	2820
GAAGAAGAAA	CTTTACGCAA	TGGACGTAAA	CAGTTAATTA	TTACTGAAAT	TCCATATGAA
CTTCTTCTTT	GAAATGCGTT	ACCTGCATTT	GTCAATTAAT	AATGACTTTA	AGGTATACTT

2830 2840 2850 2860 2870 2880  
 GTGAACAAAG GTAGCTTAGT AAAACGTATC GATGAATTAC GTGCTGACAA AAAAGTCGAT  
 CACTTGTTC CATCGAATCA TTTTGCATAG CTACTTAATG CACGACTCTT TTTTCAGCTA  
  
 2890 2900 2910 2920 2930 2940  
 GGTATCGTTG AACTACGTGA TGAACTGAT AGAACTGGTT TACGAATAGC AATTGAATTG  
 CCATAGCAAC TTCATGCACT ACTTTGACTA TCTTGACCAA ATGCTTATCG TTAACCTAAC  
  
 2950 2960 2970 2980 2990 3000  
 AAAAAAGATG TGAACAGTGA ATCAATCASA AATTATCTTT ATAAAACTC TGATTACAG  
 TTTTCTCTAC ACTTGCTACT TAGTTAGTTT TTAATAGAAA TATTTTGTAG ACTAAATGTC  
  
 3010 3020 3030 3040 3050 3060  
 ATTTTCATATA ATTTCAACAT GGTGCGTATT AGTGATGGTC GTCCAAATTT GATGGGTATT  
 TAAAGTATAT TAAAGTTGTA CCGCGGATAA TCCTACCAG CAGGTTTAA CTACCCATAA  
  
 3070 3080 3090 3100 3110 3120  
 CGTCAAATTA TAGATAGTTA TTTGAATCAT CAAATTGAGG TTGTTGCAAA TAGAACGAAG  
 GCAGTTTAAAT ATCTATCAAT AAACCTTAGTA GTTTAACTCC AACAACGTTT ATCTTGCTTC  
  
 3130 3140 3150 3160 3170 3180  
 TTTGAATTAG ATAATGCTGA AAAACGTATG CATATCGTTG AAGGTTTGAT TAAAGCGTTG  
 AAACCTTAATC TATTACGACT TTTTGCATAC GTATAGCAAC TTCCAACTA ATTCGCAAC  
  
 3190 3200 3210 3220 3230 3240  
 TCAATTTTAG ATAAAGTAAT CGAATTGATT CGTAGCTCTA AAAACAAGCG TGAGCGCTAAA  
 AGTTAAATC TATTTTATTA GCTTAACTAA GCATCGAGAT TTTTGTTCGC ACTGCGATTT  
  
 3250 3260 3270 3280 3290 3300  
 GAAAACCTTA TCGAAGTATA CGAGTTTACA GAAGAACAGG CTGAAGCAAT TGTAATGTTA  
 CTTTGTGAAT AGCTTCATAT GCTCAAGTGT CTTCTTGTCC GACTTCGTTA ACATTACAAT  
  
 3310 3320 3330 3340 3350 3360  
 CAGTTATATC GTTTAACAAA CACTGACATA GTTGCGCTTG AAGGTGAACA TAAAGAATT  
 GTCAATATAG CAAATTGTTT GTGACTGTAT CAACGCGAAC TTCCACTTGT ATTTCTTGAA  
  
 3370 3380 3390 3400 3410 3420  
 GAAGCATTAA TCAACAATT ACCTCATATT CTTGATAACC ATGATGCATT ATTGAATGTC  
 CTTCTGAATT AGTTTGTAA TGCAGTATAA GAACTATTGG TACTACGTAA TAACTTACAG  
  
 3430 3440 3450 3460 3470 3480  
 ATAAAAGAAG AATTGAATGA AATTAAAAAG AAATTCAAAT CTGAACGACT GTCTTTAATT  
 TATTTTCTTC TTAACCTTACT TTAATTTTTC TTTAAGTTTA GACTTGCTGA CAGAAATTAA  
  
 3490 3500 3510 3520 3530 3540  
 GAAGCAGAAA TTGAAGAAAT TAAATTGAC AAAGAAGTTA TGGTGCCTAG TGAAGAAGTT  
 CTTCTGCTTT AACTTCTTTA ATTTTAACTG TTTCTTCAAT ACCACGGATC ACTTCTTCAA  
  
 3550 3560 3570 3580 3590 3600  
 ATTTTAAAGTA TGACACGTCA TGGATATATT AAACGTACTT CTATTCGTAG CTTTAAATGCT  
 TAAATTCAT ACTGTGCAGT ACCTATATAA TTTGCATGAA GATAAGCATC GAAATTACGA  
  
 3610 3620 3630 3640 3650 3660  
 AGCGGTGTTG AAGATATTGG TTTAAAAGAT GGTGACAGTT TACTTAAACA TCAAGAAGTA  
 TCGCCACAAC TTCTATAACC AAATTTTCTA CCACTGTCAA ATGAATTTGT AGTTCCTCAT

3670	3680	3690	3700	3710	3720
AATACGCAAG	ATACCGTACT	AGTATTTACA	AATAAAGGTC	GTTATCTATT	TATACCAAGT
TTATGCGTTC	TATGGCATGA	TCATAAATGT	TTATTTCCAG	CAATAGATAA	ATATGGTCAA
3730	3740	3750	3760	3770	3780
CATAAATTAC	GAGATATTCG	TTGGAAAGAA	TTGGGGCAAC	ATGTATCACA	AATAGTTCCT
GTATTTAATG	CTCTATAAGC	AACCTTTCTT	AACCCCGTTG	TACATAGTGT	TTATCAAGGA
3790	3800	3810	3820	3830	3840
ATCGAAGAAG	ATGAAGTGGT	TATTAATGTC	TATAATGAAA	AGGACTTTAA	TACTGATGCA
TAGCTTCTTC	TACTTCACCA	ATAATTACAG	ATATTACTTT	TCCTGAAATT	ATGACTACGT
3850	3860	3870	3880	3890	3900
TTTTATGTTT	TTGCGACTCA	AAATGGCATG	ATTAAGAAAA	GTAAGTGGCC	TCTATTTAAA
AAAATACAAA	AACGCTGAGT	TTTACCGTAC	TAATTTCTTT	CATGTCACGG	AGATAAATTT
3910	3920	3930	3940	3950	3960
ACAACGCGTT	TTAATAAACCC	TTTAATTGCA	ACTAAAGTTA	AAGAAAATGA	TGATTTGATT
TGTTGCGCAA	AATTATTTGG	AAATTAACGT	TGATTTCAAT	TTCTTTTACT	ACTAAACTAA
3970	3980	3990	4000	4010	4020
AGTGTATATG	GCTTTGAAAA	AGATCAATTA	ATTACCGTAA	TTACAAATTA	AGGTATGTCA
TCACAATACG	CGAAACTTTT	TCTAGTTAAT	TAATGGCATT	AATGTTTATT	TCCATACAGT
4030	4040	4050	4060	4070	4080
TTAACGTATA	ATACAAGTGA	ACTATCAGAT	ACTGGATTAA	GGGCGGCTGG	TGTTAAATCA
AATTGCATAT	TATGTTCACT	TGATAGTCTA	TGACCTAATT	CCCGCCGACC	ACAATTTAGT
4090	4100	4110	4120	4130	4140
ATAAATCTTA	AAGTTGAAGA	TTTCGTTGTT	ATGACAGAAG	GTGTTTCTGA	AAATGATACT
TATTTAGAAT	TTCAACTTCT	AAAGCAACAA	TACTGTCTTC	CACAAAGACT	TTTACTATGA
4150	4160	4170	4180	4190	4200
ATATTGATGG	CCACACAACG	CGGCTCGTTA	AAACGTATTA	GTTTTAAAAA	CTTACAAGTT
TATAACTACC	GGTGTGTTGC	GCCGAGCAAT	TTTGCAATAT	CAAAATTTTA	GAATGTTCAA
4210	4220	4230	4240	4250	4260
GCTAAAAGAG	CACAACGTGG	AATAACTTTA	TTAAAAGAAT	TAAAGAAAAA	TCCACATCGT
CGATTTTCTC	GTGTTGCACC	TTATTGAAAT	AATTTTCTTA	ATTTCTTTT	AGGTGTAGCA
4270	4280	4290	4300	4310	4320
ATAGTAGCTG	CACATGTAGT	GACAGGTGAA	CATAGTCAAT	ATACATTATA	TTCAAAATCA
TATCATCGAC	GTGTACATCA	CTGTCCACTT	GTATCAGTTA	TATGTAATAT	AAGTTTITAGT
4330	4340	4350	4360	4370	4380
AACGAAGAAC	ATGGTTTAAAT	TAATGATATT	CATAAATCTG	AACAATATAC	AAATGGCTCA
TTGCTTCTTG	TACCAAATTA	ATTACTATAA	GTATTTAGAC	TTGTTATATG	TTTACCGAGT
4390	4400	4410	4420	4430	4440
TTCAATTGTAG	ATACAGATGA	TTTTGGTGAA	GTAATAGACA	TGTATATTAG	CTAAAACTA
AAGTAACATC	TATGTCTACT	AAAACCACTT	CATTATCTGT	ACATATAATC	GATTTTITGAT
4450	4460	4470	4480	4490	4500
TATGCAATCA	CGAAATTAAA	TGATAAAATA	CAGTAATGTT	AAATTTTGAC	TAAATTCAAG
ATACGTTAGT	GCTTTAATTT	ACTATTTTAT	GTCATTACAA	TTTAAACTG	ATTTAAGTTC

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      4510      4520      4530      4540      4550      4560
GGATTATAT TAAATGCTGA CCAAGTACTT ATCGTTAAAT TAGCGATACG GAATCCGCGG
CCTAAATATA ATTTACGACT GGTTCATGAA TAGCAATTGA ATCGCTATGC CTTAGGCGCC

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AATTC
TTAAG

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(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Staphylococcus aureus*

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:



M S E I I Q D L S L E D V L G D R F G R Y S K Y I  
 GTGAGTGAAATAATTCAAGATTTATCACTTGAAGATGTTTTAGGTGATCGCTTTGGAAGATATAGTAAATATATT  
 2032 2042 2052 2062 2072 2082 2092 2102  
 I Q E R A L P D V R D G L K P V Q R R I L Y A M Y  
 ATTCAGAGCGGTGCATTGCCAGATGTTCTGTGATGGTTTAAACCACTACAACGTCTATTTATACGCAATGTAT  
 2107 2117 2127 2137 2147 2157 2167 2177  
 S S G N T H D K N F R K S A K T V G D V I G O Y H  
 TCAAGTGGTAATACACACGATAAAAAATTCGGTAAAGTGCGAAACAGTGGTGATGTTATTGGTCAACATCAT  
 2182 2192 2202 2212 2222 2232 2242 2252  
 F H G D S S V Y E A M V R L S Q D W K L R H V L I  
 CCACATGGAGACTCTCTCAGTGTACGAAGCAATGGTCCGTTTAAAGTCAAGACTGGAAGTTACGACATGTCTTAATA  
 2257 2267 2277 2287 2297 2307 2317 2327  
 E M H G N N G S I D H D P P A A M R Y T E A K L S  
 GAAATGCATGGTAATAATGGTAGTATCGATAATGATCCGCCAGCGCAATGCCATTACACTGAAGCTAAGTTAAGC  
 2332 2342 2352 2362 2372 2382 2392 2402  
 L L A E E L L K D I N K E T V S F I P N Y D D T T  
 TTACTAGCTGAAGATTATTACGTGATATTAATAAAGAGACACTTCTTTTATTCCAACTATGATGATACGACA  
 2407 2417 2427 2437 2447 2457 2467 2477  
 L E F H V L F S K F F H L L V N G S T G I S A G Y  
 CTCGAACCAATGGTATTGCCATCAAGATTTCCTAACTTACTAGTGAATGGTTCTACAGGTATATCTGCAGSTTAC  
 2482 2492 2502 2512 2522 2532 2542 2552  
 A T C I F F H N L A E V I Q A T L K Y C D N P D I  
 GCGACAGATATACCACACATAATTTAGTGAAGTGATTCAAGCAACACTTAAATATATTGATAATCCGGATATT  
 2557 2567 2577 2587 2597 2607 2617 2627

T V H L L M P Y I K S F C F I T S S I I Q G : D G  
 A C A G T C A A T C A A T T A A T G A A A T A T A T T A A A G S T C T G A T T T T C C A A C T S S T G S T A T T A T T C A A G S T A T T G A T G G T  
 2631 2642 2652 2662 2672 2682 2692 2702  
 : K K A Y E S G K G R I I V R E E E E E T L R N  
 A T T A A A A A G C T T A T G A A T C A G G T A A A G S T A G A A T T A T A G T T C G T T C T A A A S T T G A A G A G A A A C T T T A C G C A A T  
 2707 2717 2727 2737 2747 2757 2767 2777  
 G R K O L : I T E I P Y E V N K S S L V K R : D E  
 G G A C G T A A A C A G T T A A T T A T T A C T G A A A T T C C A T A T G A A G T G A A C A A A S T A G T T A G T A A A A C G T A T C G A T G A A  
 2782 2792 2802 2812 2822 2832 2842 2852  
 L R A D K K V D G I V E V R D E T D R T G L R I A  
 T T A C G T G C T G A C A A A A A G T C G A T G G T A T C G T T G A A G T A C G T G A T G A A A C T G A T A G A A C T G G T T T A C C A A T A G C A  
 2857 2867 2877 2887 2897 2907 2917 2927  
 I E L K K D V N S E S I K N Y L Y K N S D L O I S  
 A T T G A A T T G A A A A A G A T G T G A A C A G T G A A T C A A T C A A A A A T T A T C T T A T A A A A C T C T G A T T T A C A G A T T T C A  
 2932 2942 2952 2962 2972 2982 2992 3002  
 Y N F N M V A I S D G R P K L M G I R Q I I D S Y  
 T A T A A T T C A C A T G G T C G T A T T A G T G A T G G T C G C A A A A T T G A T G G G T A T T C G T C A A A T T A T A G A T A G T T A T  
 3007 3017 3027 3037 3047 3057 3067 3077  
 L H M O : E V V A N R T K F E L D N A E K R M H I  
 T T G A A T C A T C A A A T T G A G G T T G T T G C A A A T A G A A C G A A G T T T G A A T T A G A T A A T G C T G A A A A C G T A T C A T A T C  
 3082 3092 3102 3112 3122 3132 3142 3152  
 V E G L I K A L S I L D K V I E L I R S S K N K R  
 G T T G A A G G T T T G A T T A A A G C G T T G T C A A T T T A G A T A A A G T A A T C G A A T T G A T T C G T A G T C T A A A A C A A G C G T  
 3157 3167 3177 3187 3197 3207 3217 3227  
 D A K E N L I E V Y E F T E E Q A E A I V M L O L  
 G A C G C T A A A G A A A A C G T T A T C G A A G T A T A C G A G T T C A C A G A A A C A G G C T G A A G C A A T T G T A A T G T T A C A G T T A  
 3232 3242 3252 3262 3272 3282 3292 3302  
 Y E L T N T D I V A L E G E N K E L E A L : K D I  
 T A T C G T T T A C A A A C A C T G A C A T A G T T G C G C T T G A A G G T G A A C A T A A A G A A C T T G A A G C A T T A A T C A A A C A A T T A  
 3307 3317 3327 3337 3347 3357 3367 3377  
 R H I L D N H D A L L N V I K E E L N E I K K K F  
 C G T C A T A T T C T T G A T A A C C A T G A T G C A T T A T T G A A T G T C A T A A A A G A A A T T G A A T G A A A T T A A A A G A A A T T C  
 3382 3392 3402 3412 3422 3432 3442 3452  
 K S E K L S L I E A E I E E I K I D K E V M V P S  
 A A A C T G A A C G A C T G T C T T A A T T G A A G C A A A T T G A A G A A A T T A A A A T T G A C A A A G A A G T A T G G T G C C T A G T  
 3457 3467 3477 3487 3497 3507 3517 3527  
 E E V I L S M T R H G Y I K R T S : R S F N A S G  
 G A A G A A S T T A T T T A A G T A T G A C A C G T C A T G G A T A T A T T A A A C G T A C T T C T A T T C G T A G C T T A A T S C T A G C G G T  
 3532 3542 3552 3562 3572 3582 3592 3602  
 V E D I G L K D G D S L L K H O E V N T O D T V L  
 G T T G A A G A T A T T G G T T A A A A G A T G G T G A C A G T T T A C T T A A A C A T C A A G A A T A A A T A C G C A A G A T A C C G T A C T A  
 3607 3617 3627 3637 3647 3657 3667 3677  
 V F T N K G R Y L F I F V H K L R E : R M K E L G  
 G T A T T T A C A A A T A A A S S T C S T A T C A T T T A T A C C A G T T C A T A A A T T A C G A A T A T T C S T T G G A A A G A A T T G G G G  
 3682 3692 3702 3712 3722 3732 3742 3752  
 Q M V S Q I V F I E E D E V V I N Y Y N E K D F N  
 C A A C A T G T A T C A C A A A T A G T T C C T A T C G A A G A A G A T G A A G T G G T T A T A A T G T T A A T G A A A A G A C T T A A T  
 3757 3767 3777 3787 3797 3807 3817 3827  
 T C A F I V F A T O N S M I K K S T V F L F K T T  
 A C T G A T G C A T T T A T G T T T T G G A C T C A A A A T S C C A T G A T T A A G A A A A T A C A S T S C C T A T T T A A A A C A A C G  
 3832 3842 3852 3862 3872 3882 3892 3902  
 K F H K E L L A T K V K E N D E L I S V M R F E K  
 C G T T T A A T A A A C C T T A A T T G C A A C T A A A G T T A A G A A A A T G A T G A T T G A T T A G T G T T A T G C G C T T T G A A A A  
 3907 3917 3927 3937 3947 3957 3967 3977

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D Q L I T A I T K K G H S L T Y K T S E L S D T G
GATCAATTAATTACCGTAATTACAAATAAAGGSTATGTGCTTAAAGTATAATACAAAGTGAATATCAGATACTGGA
3982 3992 4002 4012 4022 4032 4042 4052

L R A A G V K S I H L K V E D F V V M T E G V S E
TTAAGGGCGGCTGGTGTAAATCAATAAATCTTAAAGTTGAAGATTCTTTGTTATGACAGAAGGTGTTCTGAA
4057 4067 4077 4087 4097 4107 4117 4127

N D T I L M A T Q R G S L K K I E F K I L Q V A K
AATGATACTATATTGATGGCCACACAACGGGCTCGTTAAACGCTATTAGTTTTAAATCTTACAAGTTGCTAAA
4132 4142 4152 4162 4172 4182 4192 4202

R A Q R G I T L L K E L K K N F H R I V A A H V V
AGAGCACAACTGGGAATAACTTTATTAAAGAATTAAAGAAAAATCCACATCGTATAGTAGCTGCACATGTAGTG
4207 4217 4227 4237 4247 4257 4267 4277

T G E H S Q Y T L Y S K S N E E H G L I N D I H K
ACAGGTGAACATAGTCAATATACATTATATTCAAAATCAAACGAAGAATGGTTTAATTAATGATATTCAAAA
4282 4292 4302 4312 4322 4332 4342 4352

S E Q Y T N G S F I V D T D D F G E V I D N Y I S
TCTGAACAATATACAAATGGCTCATTGATGTAGATACAGATGATTTTGGTGAAGTAATAGACATGTATATTAGC
4357 4367 4377 4387 4397 4407 4417 4427

...
TAA
4432

```

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1991 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

10 (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Staphylococcus aureus*

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

M N K C K N Y S D D S I Q V L E S L E A V R K R F  
 ATGATATAACAAATATATTATTCAGATGATTCAATACAGSTTTTAGAGGGSTTAGAAGCAGTTTCGTAAAAGACCT  
 41 51 61 71 81 91 101 111  
 G M Y I G S T C K R G L H N L V Y E E V D N S V D  
 GSTATGTATATTGGATCAACTGATAAACGGGGATTACATCATCTAGTATATGAAATTGTGATAACTCGGTGGAT  
 116 126 136 146 156 166 176 186  
 E V L N G Y G H E I C V T I N I C G S I S I E D H  
 GAAGTATTGAATGGTTACGGTAAGGAAATAGATGTAACAACTAATAAGGATGGTATATTCTATAGAAGATAAT  
 191 201 211 221 231 241 251 261  
 G R G M F T G I H K S G K F T V E V I F T V L H A  
 GGACGTGGTATGCCAACAGGTATACATAAATCAGSTAAACGGACAGTGGAACTTATCTTTACTGTTTACATGCA  
 266 276 286 296 306 316 326 336

T G N F S C I E Y P T S G G L H G V G R E A V N A  
 GGAGGTAAATTTGGACAAAGTCTTATATAAACTTCAGGTGGTCTTCAGCGCGTTGGTGGTTCAGTGGTAAATGCA  
 341 351 361 371 381 391 401 411  
 L S E W L E V E I H R D G N I Y H Q S F H N G G S  
 TTGAGTGAATGGCTTGAAGTTGAATCCATCGAGATGGTAATATATATCATCAAAGTTTAAACCGGTGGTTCG  
 416 426 436 446 456 466 476 486  
 P S S G L V K N G K T K K T G T K V T F K P D D T  
 CCATCTTCAGGTTTASTGAAAAGGTAAACTAAGAAAACAGGTACCAAAGTAACATTTAAACCTGATGACACA  
 491 501 511 521 531 541 551 561  
 I F K A S T S E N F D V L S E R L Q E S A F L L K  
 ATTTTAAAGCATCTACATCATTAAATTTTGGTGGTAAAGTGAACGACTACAAGAGTCTCGGTCTTATTGAAA  
 566 576 586 596 606 616 626 636  
 N L K I T L N E L R S G K E R Q E H Y H Y E E G I  
 AATTTAAATAACGCTTAATTTTACCGAGTGGTAAAGAGCGTCAAGAGCATTACCATTTATGAAGGAAGTATC  
 641 651 661 671 681 691 701 711  
 K E F V S Y V H E G K E V L H D V A T F S G E A N  
 AAAGAGTTTGTAGTTATGTCATGAAGGAAAGAGTTTTCATGAGGTGGCTACATTTTCAGGTGAAGCAAT  
 716 726 736 746 756 766 776 786  
 G I E V C V A F Q Y N D O Y S E S I L S F V N N V  
 GGTATAGAGGTAGACGTAGCTTTTCAATATAATGATCATATTGAGAAAGTATTTTAAAGTTTGTAAATAATGTA  
 791 801 811 821 831 841 851 861  
 R T K D C G T H E V G F K T A M T R V F N D Y A R  
 CGTACTAAAGATGGTGGTACATGAAAGTTTGGTAAACAGCAATGACACGCGTATTTAATGATTATGCGCGT  
 866 876 886 896 906 916 926 936  
 R I N E L K T F D K N L D G N D I R E G L T A V V  
 CGTATTAAAGAACTTAAACAAAGATAAACAACTTAGATGGTAATGATATTGCTGAAGGTTTAAAGGTGTTGTG  
 941 951 961 971 981 991 1001 1011  
 S V R I F E E L L O F E G Q T H S K L G T S E A R  
 TCTGTTGCTATTCAGAAAGATTTATGCAATTTGAAGGACAAACGAAATCTAAATGGGTACTTCTGAAGGTAGA  
 1016 1026 1036 1046 1056 1066 1076 1086  
 S A V F S V V A D K I P F Y L E E K G Q L S K S L  
 AGTGCTGTTGATTGAGTTGTTGAGACAAATGGCAATCTATTAGAAGAAAAGGACAAATGCTAAATCACTT  
 1091 1101 1111 1121 1131 1141 1151 1161  
 V K K A I K A Q Q A R E A A R K A R E D A R S G K  
 GTGAAAAAGCGATTAAAGCACACAAAGCAAGGGAAGGTGCACGTAAGCTCGTGAAGATGCTCCTTCAGGTAAAG  
 1166 1176 1186 1196 1206 1216 1226 1236  
 K N H R F D T L L S G K L T P A Q S K N T E K N E  
 AAAACAAAGCGTAAAGACACTTTCTATCTGGTAAATTAACACCTGCACAAAGTAAACAACTGAAAAAATGAA  
 1241 1251 1261 1271 1281 1291 1301 1311  
 L Y L V E G S D C A G G S A K L G R D R K F Q A I L  
 TTGTATTTAGTGAAGGTGATTCTGGGGAGGTTGAGCAAACTTGGACGAGACCGCAATTTCAAGCGATATTA  
 1316 1326 1336 1346 1356 1366 1376 1386  
 P L R G V Y I N T E K A R L E C I F K H E E I N T  
 CCATTACGTGGTAAGGTAAATTAACAGAGAAAGCACTCTAGAAGATATTTTAAATTAAGAAATTAATACA  
 1391 1401 1411 1421 1431 1441 1451 1461  
 I I H T I G A S V G T D F K I E D S N Y N R V I I  
 ATTATCCACACAAATCGGGCAAGCGTTGGTACTGACTTAAATTAAGATAGTAATTTATATCCTGTAATTTAT  
 1466 1476 1486 1496 1506 1516 1526 1536  
 M T F A T T E S A N I Q V L L L T F F F F H Y M Y F  
 ATGACTGATGGTGAATTTGATTTGGCGCATATTCAGGTGCTATTGTTAACTTTCTTCAATATATGAACCG  
 1541 1551 1561 1571 1581 1591 1601 1611  
 L V Q A S R V F I A L P F L Y E L E H S K G K T K  
 CTTGTTCAAGCAAGTCTGTATTTATTTGTTTACCTCCACTTTATAAATTTGAAAAAGTTAAAGGCAAAACAAAG  
 1616 1626 1636 1646 1656 1666 1676 1686

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K V E Y A W T C E E L N K L Q N E L S K G F T L Q
CGAGTTGAATACGGTTGGACAGACGAAGAGCTTAATAAATTGCAAAAGAACTTCGTAAGGCTTCACGTTACAA
1731      1741      1751      1761      1771      1781      1791      1801

R Y K G L G E M N F E Q L W E T T M N F E T R T L
CGTTACAAAGGTTTGGGTGAAATGAACCTGAAACAATTATGGGAAACGAGGATGAACCCAGAAACACGAACTTTA
1766      1776      1786      1796      1806      1816      1826      1836

I R V Q V E D E V A S S K R V T T L M G D N V Q F
ATTTCGTGTACAAGTTGAAGATGAAGTCCGTTTCATCTAAACGTGTAAACAACATTAAATGGGTGACAAAGTACAACCT
1841      1851      1861      1871      1881      1891      1901      1911

R R E W I E N H V E F G M Q E D Q S I L D N S E V
AGACGTGAATGGATTGAAAAGCATGTTGAGTTTGGTATGCAAGAGGACCAAAGTATTTAGATAATTCTGAAGTA
1916      1926      1936      1946      1956      1966      1976      1986

Q V L E N D Q F D E E E I ***
CAAGTGGTTGAAAATGATCAATTTGATGAGGAGGAAATCTAG
1991      2001      2011      2021

```

## (5) INFORMATION FOR SEQ ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTISENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGCGAATTC GATGGWYTWA AACCWGTWCA

## (6) INFORMATION FOR SEQ ID NO: 5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTISENSE: YES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

10

CGCGAAGCTT TTCWGTATAW CKCATWGCWG C

## (7) INFORMATION FOR SEQ ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCGAATTC TWCATGCWGG WGGWAAATT

(8) INFORMATION FOR SEQ ID NO: 7:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CGCGAAGCTT WCCWCCWGCW GAATCWCCTT C

15 (9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids



(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Met Arg Tyr Thr Glu

5

(10) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Tyr His Pro His Gly Asp S r

5

## (11) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iii) ANTISENSE: NO

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGCGGATCCC ATATGGCTGA ATTACCTCA

## (12) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: lin ar

15

## (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCGGAATTC GACGGCTCTC TTTCATTAC

5 (13) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

15 GGCCGGATCC CATATGAGTG AAATAATTCA AGATT

(14) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

10

GGCCGAATTC TAATAATTAA CTGTTTACGT CC

## (15) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTISENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGCCGAGCTC CAATTCTTCT TTTATGACAT TC